```
CGCGATCGTC GTCAACGANG TCGACCGTCA CCACGGACTG ATCAACAAGT TCGCAGGCGA      60
CGCCGCCCTG GCCATCTTCG GAGCCCCGAA CCGCCTCGAC CGTCCCCAAG ACGCCGCGCT     120
GGCCGCCGCC CGGGCCATAN CCGANCCGCT GGCCNACGAG ATGCCCGAGG TCCAAGCCGG     180
CATCGGGGTG GCGCCAGGCC ANATCGTCGC CGGCAATGTC GGCGCCAAGC AAAGATTCNA     240
ATACACAGTG GTCGGCAAGC CGGTCAACCA NGCGGCCCGA TTGTGCGAAC TGGCCAAATC     300
ACACCCCGCG CGATTGGGTC TCGCCCGCTC GGCTCATGGT CACCCAATTC AAGGACTACT     360
TTGGCCTGGC GCACGACCTG CCGAAGTGGG CGAGTGAAGG CGCCAAAGCC GCCGGTGACG     420
CCGCCAAGGC GTTGCCGGCC GCCGTTCCGG CCATTCCGAG TGCTGGCCTG AGCGGCGTTG     480
CGGGCGCCGT CGGTCAGGCG GCGTCGGTCG GGGGATTGAA GGTTCCGGCC GTTTGGACCG     540
CCACGACCCC GCCGGCGAGC CCCGCGGTGC TGGCGGCGTC CAACGGCCTC GGAGCCGCGG     600
CCGCCGCTGA AGGTTCGACA CACGCGTTTG GCGGGATGCC GCTCATGGGT ANCGGTGCCG     660
GACGTGCGTT TAACAACTTC GCTGCCCCTC GATACGGATT CAAGCCGACC GTGATCGCCC     720
AACCGCCGGC TGGCGGATGA CCAACTACGT TCGTTGATCG AGGATCGAAT TCNACGATTC     780
AAAGGGAGGA ATTCATATGA CCTCNCGTTT TATGACCGAT CCGCACGCNA TNCGGGACAT     840
GGCGGGCCGT TTTGAGGTGC ACGCCCAGAC GGTGGAGGAC GAGGCTNGCN GGATGTGGGC     900
GTCCCGCCAA AACATTTCCG GTGCGGGCTG GAGTGGCATG GCCGAGCCGA CCTCGNTACA     960
CACCATGGCC CAGATGAATC AGGCGTTTCN CAACATCGTG AACATCCTGC ACGGGGTGNG    1020
TGACGGGCTG GTTCGCGACG CCAACAACTA CGAACAGCAA GAGCAGGCCT CCCAGCAGAT    1080
CCTCAGCAGC TGACCCCGCC CGACGACTCA GGAGGACACA TGACCATCAA CTATCAATTC    1140
GGCGACGTCG ACGCTCATGG CGCCATGATC CGCCCTNTGG CCGGGTTGCT GGAGGCCGAG    1200
CATCAGGCCA TCATTTCTGA TGTGTTGACC GCGAGTGACT TTTGGGGCGG CGCCGGTTCG    1260
GCGGCCTGCC AGGGGTTCAT TACCCAGTTG GGCCGTAACT TCCAGGTGAT TTACGAGCAG    1320
GCCAACGCCC AGGGGCAGAA GGTGCAGGCT GCCGGCAACA ACATGGCACA AACCGACAGC    1380
GCCGTNGGNT CCAGCTGGGC CTAACCCGGG TCNTAAGTTG GGTCCGCGCA GGGCGGGCCG    1440
ATCAGCGTNG ACTTTGGCGC CCGATACACG GGCATNTTNT NGTCGGGAAC ACTGCGCCCG    1500
CGTCANNTGC CCGCTTCCCC TTGTTNGGCG ACGTGCTCGG TGATGGCTTT GACGACCGCT    1560
TCGCCGGCGC GGCCAATCAA TTGGTCGCGC TTGCCTNTAG CCCATTCGTG CGACGCCCGC    1620
GGCGCCGCGA GTTGTCCCTT GAAATAAGGA ATCACAGCAC GGGCGAACAG CTCATAGGAG    1680
TGAAAGGTTG CCGTNGCGGG GCCC                                           1704
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
CCGTCTTGGC GTCTGGGCGC ATTGTGATCT GGGCCANTTG CCCCTCCACC CAGACCGCGC      60
CCAGCTTGTC GATCCAGCCC GCGACCCGGA TTGCCACCGC GCGAACCGGG AACGGATTCT     120
CCGCTGAATT CTGGGTCACT TCGCAGTCGC GCGGGTGATC CTGTTGGCGA NCAGCGTCTG     180
GAACGGGCGT CNAACGCGTG CCGTAAGCCC AGCGTNTACN CCGTCAGCCC GACGCCGATG     240
CCGAATGCCT TGCCGCCCAA GCTGAGCCGC GCGGGCTCCA CCAAGAGCGT CACGGTGAGC     300
CAGCCAACCA GATGCAAGGC GACGATCACC GCGAAGTGCC GAATTCGGCA CGAGAGGTGC     360
TGGAAAATCC A GCAATACGCC CGCGAGCCGA TCTCGTTGGA CCAGACCATC GGCGACGANG     420
GCGACAGNCA GCTTGGCGAT TTCATCGAAA ACAGCGAGGC GGTGGTGGNC GTCGACGCGG     480
TGTCCTTCAC TTTGCTGCAT GATCAACTGC ANTCGGTGCT GGACACGCTC TCCGAGCGTG     540
AGGCGGGCGT GGTGCGGCTA CGCTTCGGCC TTACCGACGG CCAGCCGCGC ACCCTTGACG     600
AGATCGGCCA GGTCTACGGC GTGACCCGGG AACGCATCCG CCAGATCGAA TCCAAGACTA     660
TGTCGAAGTT GCGCCATCCG AGCCGCTCAC AGGTCCTGCG CGACTATCGT GCCGAATTCG     720
GCACGAGCCG TTTTGAGGTG CACGCCCAGA CGGTGGAGGA CGAGGCTCGC CGGATGTGGG     780
CGTCCGCGCA AAACATTTCC GGTGCGGGCT GGAGTGGCAT GGCCGAGCCG ACCTCGCTAG     840
ACACCATGGC CCAGATGAAT CAGGCGTTTC GCAACATCGT GAACATGCTG CACGGGGTGC     900
GTGACGGGCT GGTTCGCGAC GCCAACAACT ACGAACAGCA AGAGCAGGCC TCCCAGCAGA     960
```

```
TCCTCAGCAG CTGACCCGGC CCGACGACTC AGGACGACAC ATGACCATCA ACTATCAATT    1020
CGGGGACGTC GACGCTCATG GCGCCATGAT CCGCCCTCTG GCCGGCTTGC TGGAGGCCGA    1080
GCATCAGGCC ATCATTTCTG ATGTGTTGAC CGCGAGTGAC TTTTGGGGCG GCGCCGGTTC    1140
GGCGGCCTGC CAGGGTTCA TTACCCAGTT GGGCCGTAAC TTCCAGGTGA TCTACGAGCA    1200
GGCGAACGCC CACGGGCAGA AGTTGCAGGC TGCCGGCAAC AACATGGCAC AAACCGACAG    1260
CGCCGTCGGC TCCAGCTGGG CCTAACCCGG GTCCTAAGTT GGGTCCGCGC AGGGCGGGCC    1320
GATCAGCGTC GACTTTGGCG CCCGATACAC GGGCATGTNG TNGTCGGGAA CACTGCGCCC    1380
GCGTCAGCTG CCCGCTTCCC CTTGTTCGGC GACGTGCTCG GTGATGGCTT TGACGACCGC    1440
TTCGGCGGCG CGGCCAATCA ATTGGTTCGCG CTTGCCTCTA GCCTCGTGCC GAATTCGGCA    1500
CGAGGGTGCT GGTGCCGCGC TATCGGCAGC ACGTGAGCTC CACGACGAAC TCATCCCAGT    1560
GCTGGGTTCC GCGGAGTTCG GCATCGGCGT GTCGGCCGGA AGGGCCATCG CCGGCCACAT    1620
CGGCGCTCAA GCCCCGCTTC GATACACCGT CATCGGCGAC CCGGTCAACG AGGCCGCCCG    1680
GCTCACCGAA CTGGCCAAAG TCGAGGATGG CCACGTTCTG GCGTCGGCGA TCGCGGTCAG    1740
TGGCGCCCTG GACGCCGAAG CATTGTGTTG GGATGTTGGC GAGGTGGTTG AGCTCCGCGG    1800
ACGTGCTGCA CCCACCCAAC TAGCCAGGCC AATGAATNTG GCNGCACCCG AAGAGGTTTC    1860
CAGCGAAGTA CGCGGCTAGT CGCGCTTGGC TGCNTTCTTC GCCGGCACCT TCCGGGCAGC    1920
TTTCCTGGCT GGCCGTTTTG CCGGACCCCG GGCTCGGCGA TCGGCCAACA GCTCGGCGGC    1980
GCGCTCGTCG GTTATGGAAG CCACGTNGTC GCCCTTACGC AGGCTGGCAT TGGTCTCACC    2040
GTCGGTGACG TACGGCCCGA ATCGGCCGTC CTTGATGACC ATTGGCTTGC CAGACGCCGG    2100
ATNTGNTCCC AGCTCGCGCA GCGGCGGAGC CGAAGCGCTT TGCCGGCCAC GACNTTCCGG    2160
CTCTGNGTAG ATNTTCAGGG CTTCGTCGAG CGNGATGGTG AATATATGGT CTTCGGTGAC    2220
CAGTGATCGA GAATCGTTGC CGCGCTTTAG ATACGGTCNG TAGCGCCCGT TCTGCGCGGT    2280
GATNTC                                                               2286
```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
GGGCATCTTC CCCGACCGCG CCTCGATCAT CCGCCTCGTC GGAGCCGTCC TCGCCGAACA      60
ACACGACGAA TGGATCGAAG GACGGCGCTA CCTGGGCCTC GAGGTCCTCA CCCGAGCCCG     120
AGCAGCACTG ACCAGCACCG AAGAACCGCC AAGCAGCAAA CCACCAACAC CCCAGCACTG     180
ACCACCTAGA CTGCCACCCG AAGGATCACG CGAGGAACCT TCACTCGTAC ACCACGTCCC     240
TGGCCTTGGC CTGGTGTCAG GCCCAGCTGG AGCCGACGGC GCTGTCGGTT TGCGCCATGT     300
TGTTGCCGGC AGCCTGCACC TTCTGCCCGT GGGCGTTGGC CTGCTCGTAG ATCACCTGGA     360
AGTTACGGCC CAACTGGGTA ATGAACCCCT GGCAGGCCGC CGAACCGGCG CCGCCCCAAA     420
AGTCACTCGC GGTCAACACA TCACGAATGA TGGCCTGATG CTCGGCCTCC AGCAACCCGG     480
CCTGAGCGCG GATCATGGCG CCGTGAGCGT CGACATCACC GAACTGATAG TTGATGGTCA     540
TCGAAACTGT TCTCCTTCGC TTGTAAAAGT ATTGTGCTGC AGCGGCTGAC GTTAGCTGCT     600
GAGGATCTGC TGGGAGGCCT GCTCTTGCCT CGTGCCGAAT TCGGCACGAG AGGCCGCCTT     660
CGAAGAAATC CTTTGAGAAT TCGCCAAGGC CGTCGACCCA GCATGGGTTC AGCTCGCCAG     720
CCGCGCCGGC TGGCAACCGT TCCCGCTCGA GAAAGACCTG GAGGAATACC AGTGACAAAC     780
GACCTGCCAG ACGTCCGAGA GCGTGACGGC GGTCCACGTC CCGCTCCTCC TGCTGGCGGG     840
CCACGCTTGT CAGACGTGTG GGTTTACAAC GGGCGGGCGT ACGACCTGAG TGAGTGGATT     900
TCCAAGCATC CCGCCGGCGC CTTNTTCATT GGGCGGACCA AGAACCGCGA CATCACCGCA     960
ATCGTCAAGT CCTACCATCG TGATCCGGCG ATTGTCGAGC GAATCCTGCA GCGGAGGTAC    1020
GCGTTGGGCC GCGACGCAAC CCCTAGGGAC ATCCACCCCA AGCACAATGC ACCGGCNTTT    1080
CTGTTCAAAG ACGACTTCAA CNGCTGGCGG GACACCCCGA AGTATCGATT NGACGA        1136
```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 967 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGAGCGCCAA CCCTACCGTC GGTTCGTCAC ACGGACCGCA TGGCCTGCTC CGCGGACTGC 60
CGCTAGGGTC GCGGATCACT CGGCGTAGCG GCGCCTTTGC CCACCGATAT GGGTTCCGTC 120
ACAGTGTGGT TGCCCGCCCG CCATCGGCCG GATAACGCCA TGACCTCAGC TCGGCAGAAA 180
TGACAATGCT CCCAAAGGCG TGAGCACCCG AAGACAACTA AGCAGGAGAT CGCATGCCGT 240
TTGTGACTAC CCAACCAGAA GCACTGGCGG CGGCGGCCGG CAGTCTGCAG GGAATCGGCT 300
CCGCATTGAA CGCCCAGAAT GCGGCTGCGG CGACTCCCAC GACGGGGGTG GTCCGGCGGC 360
CGCCGATGAA ATGTCCGCGC TGACGGCGGC TCAGTTCGCG GCACACGCCC AGATCTATCA 420
GGCCGTCAGC GCCCAGGCCG CGGCGATTCA CGAGATGTTC GTCAACACTC TACAGATGAG 480
CTCAGGGTCG TATGCTGCTA CCGAGGCCGC CAACGCGGCC GCGGCCGGAT AGAGGAGTCA 540
CTGCGATGGA TTTTGGGGCG TTGCCGCCGG AGGTCAATTC GGTGCGGATG TATGCCGTTC 600
CTGGCTCGGC ACCAATGGTC GCTGCGGCGT CGGCCTGGAA CGGGTTGGCC GCGGAGCTGA 660
GTTCGGCGGC CACCGGTTAT GAGACGGTGA TCACTCAGCT CAGCAGTGAG GGGTGGCTAG 720
GTCCGGCGTC AGCGGCGATG GCCGAGGCAG TTGCGCCGTA TGTGGCGTGG ATGAGTGCCG 780
CTGCGGCGCA AGCCGAGCAG GCGGCCACAC AGGCCAGGGC CGCCGCGGCC GCTTTTGAGG 840
CGGCGTTTGC CGCGACGGTG CCTCCGCCGT TGATCGCGGC CAACCGGCCT TCGTTGATGC 900
AGCTGATCTC GACGAATGTC TTTGGTCAGA ACACCTCGGC GATCGCGGCC GCCGAAGCTC 960
AGTACGG 967

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 585 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGGATTCCGA TAGCGGTTTC GGCCCCTCGA CGGGCGACCA CGGCGCGCAG GCCTCCGAAC 60
GGGGGGCCGG GACGCTGGGA TTCGCCGGGA CCGCAACCAA AGAACGCCGG GTCCGGGCGG 120
TCGGGCTGAC CGCACTGGCC GGTGATGAGT TCGGCAACGG CCCCCGGATC CCGATGGTGC 180
CGGGGACCTG GCAGCAGGGC AGCAACGAGC CCGAGGCGCC CGACGGATCG GGGAGAGGGG 240
GAGGCGACGG CTTACCGCAC GACAGCAAGT AACCGAATTC CGAATCACGT GGACCCGTAC 300
GGGTCGAAAG GAGAGATGTT ATGAGCCTTT TGGATGCTCA TATCCCACAG TTGGTGGCCT 360
CCCAGTCGGC GTTTGCCGCC AAGGCGGGGC TGATGCCGCA CACGATCGGT CAGGCCGAGC 420
AGGCGGCGAT GTCGGCTCAG GCGTTTCACC AGGGGGAGTC GTCGGCGGCG TTTCAGGCCG 480
CCCATGCCCG GTTTGTGGCG GCGGCCGCCA AAGTCAACAC CTTGTTGGAT GTCGCGCAGG 540
CGAATCTGGG TGAGGCCGCC GGTACCTATG TGGCCGCCGA TGCTG 585

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
Ala Leu Val Thr Thr Asn Phe Phe Gly Val Asn Thr Ile Pro Ile Ala
1               5                  10                  15
Leu Asn Glu Ala Asp Tyr Leu Arg Met Trp Ile Gln Ala Ala Thr Val
            20                  25                  30
Met Ser His Tyr Gln Ala Val Ala His Glu Ile Trp Cys Leu His Glu
        35                  40                  45
Xaa Ala Ser Ser Gly Lys Pro Trp Ala Ser Ile Thr Thr Gly Ala Pro
    50                  55                  60
Gly Ser Pro Ala Ser Thr Thr Arg Ser Arg Thr Pro Leu Val Ser Thr
65                  70                  75                  80
Asn Arg Xaa Val Xaa Ala Pro Ile Val Ser Pro Asn His Thr Gly His
                85                  90                  95
Arg Pro Glu Lys Gly Leu Gly Ser Xaa Gln Arg Arg Leu Ser Arg Val
            100                 105                 110
Leu Pro Arg Ile Ile Asp Arg Pro Ala Gly Pro Xaa Gly Pro Pro Leu
        115                 120                 125
Thr Ser Gly Ser His Phe Leu Cys Ser Trp His Gly Tyr Ser Ser Gln
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
His Ala Leu Ala Ala Gln Tyr Thr Glu Ile Ala Thr Glu Leu Ala Ser
1               5                  10                  15
Val Leu Ala Ala Val Gln Ala Ser Ser Trp Gln Gly Pro Ser Ala Asp
            20                  25                  30
Arg Phe Val Val Ala His Gln Pro Phe Arg Tyr Trp Leu Thr His Ala
        35                  40                  45
Ala Thr Val Ala Thr Ala Ala Ala Ala Ala His Xaa Thr Ala Ala Ala
    50                  55                  60
Gly Tyr Thr Ser Ala Leu Gly Gly Met Pro Thr Leu Ala Glu Leu Ala
65                  70                  75                  80
Ala Asn His Ala Met His Gly Ala Leu Val Thr Thr Asn Phe Phe Gly
                85                  90                  95
Val Asn Thr Ile Pro Ile Ala Leu Asn Glu Ala Asp Tyr Leu Arg Met
            100                 105                 110
Trp Ile Gln Ala Ala Thr Val Met Ser His Tyr Gln Ala Val Ala His
        115                 120                 125
Glu Ser Val Ala Ala Thr Pro Ser Thr Pro Pro Ala Pro Gln Ile Val
    130                 135                 140
Thr Ser Ala Ala Ser Ser Ala Ala Ser Ser Ser Phe Pro Asp Pro Thr
145                 150                 155                 160
Lys Leu Ile Leu Gln Leu Leu Lys Asp Phe Leu Glu Leu Leu Arg Tyr
                165                 170                 175
```

```
Leu Ala Val Glu Leu Leu Pro Gly Pro Leu Gly Asp Leu Ile Ala Gln
                180                 185                 190
Val Leu Asp Trp Phe Ile Ser Phe Val Ser Gly Pro Val Phe Thr Phe
            195                 200                 205
Leu Ala Tyr Leu Val Leu Asp Pro Leu Ile Tyr Phe Gly Pro Phe Ala
        210                 215                 220
Pro Leu Thr Ser Pro Val Leu Leu Pro Ala Val Glu Leu Arg Asn Arg
225                 230                 235                 240
Leu Lys Thr Ala Thr Gly Leu Thr Leu Pro Pro Thr Val Ile Phe Asp
                245                 250                 255
His Pro Thr Pro Thr Ala Val Ala Glu Tyr Val Ala Gln Gln Met Ser
            260                 265                 270
Gly Ser Arg Pro Thr Glu Ser Gly Asp Pro Thr Ser Gln Val Val Glu
        275                 280                 285
Pro Ala Arg Ala Glu Phe Gly Thr Ser Ala Val His Gln Ile Pro Pro
    290                 295                 300
Arg Pro Ala Asp Thr Arg Arg Ala Cys Arg His Arg Asp Asp Val Pro
305                 310                 315                 320
Arg Asp Ser Arg Ile Ala Gln His Arg Asp Gly Ala Gly Leu Asp Pro
                325                 330                 335
Thr Glu Arg Gly Thr Ser Glu Gly Asp Gln Gly Leu Val Ser Gly Trp
            340                 345                 350
```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
Met Asp Phe Gly Ala Leu Pro Pro Glu Val Asn Ser Val Arg Met Tyr
1               5                  10                  15
Ala Val Pro Gly Ser Ala Pro Met Val Ala Ala Ala Ser Ala Trp Asn
            20                  25                  30
Gly Leu Ala Ala Glu Leu Ser Ser Ala Ala Thr Gly Tyr Glu Thr Val
        35                  40                  45
Ile Thr Gln Leu Ser Ser Glu Gly Trp Leu Gly Pro Ala Ser Ala Ala
    50                  55                  60
Met Ala Glu Ala Val Ala Pro Tyr Val Ala Trp Met Ser Ala Ala Ala
65                  70                  75                  80
Ala Gln Ala Glu Gln Ala Ala Thr Gln Ala Arg Ala Ala Ala Ala Ala
                85                  90                  95
Phe Glu Ala Ala Phe Ala Ala Thr Val Pro Pro Pro Leu Ile Ala Ala
            100                 105                 110
Asn Arg Ala Ser Leu Met Gln Leu Ile Ser Thr Asn Val Phe Gly Gln
        115                 120                 125
Asn Thr Ser Ala Ile Ala Ala Ala Glu Ala Gln Tyr Gly
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
Met Ala Ser Arg Phe Met Thr Asp Pro His Ala Met Arg Asp Met Ala
1               5                  10                  15
Gly Arg Phe Glu Val His Ala Gln Thr Val Glu Asp Glu Ala Arg Arg
            20                  25                  30
Met Trp Ala Ser Ala Gln Asn Ile Ser Gly Ala Gly Trp Ser Gly Met
        35                  40                  45
Ala Glu Ala Thr Ser Leu Asp Thr Met Thr
    50                  55
```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
1               5                  10                  15
Ile Arg Ala Gln Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val
            20                  25                  30
Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val
        35                  40                  45
Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
    50                  55                  60
Tyr Glu Gln
65
```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
Met Ala Ser Arg Phe Met Thr Asp Pro His Ala Met Arg Asp Met Ala
1               5                  10                  15
Gly Arg Phe Glu Val His Ala Gln Thr Val Glu Asp Glu Ala Arg Arg
            20                  25                  30
Met Trp Ala Ser Ala Gln Asn Ile Ser Gly Ala Gly Trp Ser Gly Met
        35                  40                  45
Ala Glu Ala Thr Ser Leu Asp Thr Met Thr
    50                  55
```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
1               5                  10                  15
Ile Arg Ala Gln Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val
            20                  25                  30
Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val
        35                  40                  45
Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
    50                  55                  60
Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
```

```
65                  70                  75                  80
Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
Asn Met Leu His Gly Val Arg Asp Gly Leu Val Arg Asp Ala Asn Asn
1               5                  10                  15
Tyr Glu Gln Gln Glu Gln Ala Ser Gln Gln Ile Leu Ser Ser
            20                  25                  30
```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
1               5                  10                  15
Ile Arg Ala Gln Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
            20                  25                  30
Arg Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
        35                  40                  45
Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
    50                  55                  60
Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
65                  70                  75                  80
Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
Ala Arg Arg Met Trp Ala Ser Ala Gln Asn Ile Ser Gly Ala Gly Trp
1               5                  10                  15
Ser Gly Met Ala Glu Ala Thr Ser Leu Asp Thr Met Ala Gln Met Asn
            20                  25                  30
Gln Ala Phe Arg Asn Ile Val Asn Met Leu His Gly Val Arg Asp Gly
        35                  40                  45
Leu Val Arg Asp Ala Asn Asn Tyr Glu Gln Gln Glu Gln Ala Ser Gln
    50                  55                  60
Gln Ile Leu Ser Ser
65
```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
1               5                  10                  15
Ile Arg Ala Gln Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
            20                  25                  30
Arg Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
        35                  40                  45
Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
    50                  55                  60
Tyr Glu Gln Ala Asn Thr His Gly Gln Lys Val Gln Ala Ala Gly Asn
65                  70                  75                  80
Asn Met Ala Gln Thr Asp Ser Ala Val Xaa Ser Ser Trp Ala
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
Gly Met Ala Glu Ala Thr Ser Xaa Asp Thr Met Thr Gln Met Asn Gln
1               5                  10                  15
Ala Phe Arg Asn Ile Val Asn Met Leu His Gly Val Arg Asp Gly Leu
            20                  25                  30
Val Arg Asp Ala Asn Xaa Tyr Glu Gln Gln Glu Gln Ala Ser Gln Gln
        35                  40                  45
Ile Leu Ser Ser
    50
```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
1 5 10 15
Ile Arg Ala Gln Ala Gly Ser Leu Glu Ala Glu His Gln Ala Ile Ile
20 25 30
Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
35 40 45
Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Xaa
50 55 60
Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
65 70 75 80
Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
85 90

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 98 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Thr Ser Arg Phe Met Thr Asp Pro His Ala Met Arg Asp Met Ala
1 5 10 15
Gly Arg Phe Glu Val His Ala Gln Thr Val Glu Asp Glu Ala Arg Arg
20 25 30
Met Trp Ala Ser Ala Gln Asn Ile Ser Gly Ala Gly Trp Ser Gly Met
35 40 45
Ala Glu Ala Thr Ser Leu Asp Thr Met Ala Gln Met Asn Gln Ala Phe
50 55 60
Arg Asn Ile Val Asn Met Leu His Gly Val Arg Asp Gly Leu Val Arg
65 70 75 80
Asp Ala Asn Asn Tyr Glu Gln Gln Glu Gln Ala Ser Gln Gln Ile Leu
85 90 95
Ser Ser

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
1               5                  10                  15
Ile Arg Ala Xaa Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
            20                  25                  30
Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
        35                  40                  45
Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
    50                  55                  60
Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
65                  70                  75                  80
Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
Arg Phe Glu Val His Ala Gln Thr Val Glu Asp Glu Ala Arg Arg Met
1               5                  10                  15
Trp Ala Ser Ala Gln Asn Ile Ser Gly Ala Gly Trp Ser Gly Met Ala
            20                  25                  30
Xaa Ala Thr Ser Leu Asp Thr Met Ala Gln Met Asn Gln Ala Phe Arg
        35                  40                  45
Asn Ile Val Asn Met Leu His Gly Val Arg Asp Gly Leu Val Arg Asp
    50                  55                  60
Ala Asn Asn Tyr Glu Gln Gln Glu Gln Ala Ser Gln Gln Ile Leu Ser
65                  70                  75                  80
Ser
```

(3) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```
Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
1               5                  10                  15
Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
            20                  25                  30
Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
```

```
          35                  40                  45
Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
    50                  55                  60
Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
65                  70                  75                  80
Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```
Gln Glu Gln Ala Ser Gln Gln Ile Leu Ser Ser
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```
Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
1               5                   10                  15
Ile Arg Ala Gln Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
            20                  25                  30
Arg Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
        35                  40                  45
Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
    50                  55                  60
Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
65                  70                  75                  80
Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```
Met Ser Phe Val Thr Thr Gln Pro Glu Ala Leu Ala Ala Ala Ala Ala
1               5                  10                  15
Asn Leu Gln Gly Ile Gly Thr Thr Met Asn Ala Gln Asn Ala Ala Ala
            20                  25                  30
Ala Ala Pro Thr Thr Gly Val Val Pro Ala Ala Ala Asp Glu Val Ser
        35                  40                  45
Ala Leu Thr Ala Ala Gln Phe Ala Ala His Ala Gln Met Tyr Gln Thr
    50                  55                  60
Val Ser Ala Gln Ala Ala Ala Ile His Glu Met Phe Val Asn Thr Leu
65                  70                  75                  80
Val Ala Ser Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala Ala
                85                  90                  95
Ala Ala Gly
```

(3) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
Met Ser Phe Val Thr Thr Gln Pro Glu Ala Leu Ala Ala Ala Ala Ala
1               5                  10                  15
Asn Leu Gln Gly Ile Gly Thr Thr Met Asn Ala Gln Asn Ala Ala Ala
            20                  25                  30
Ala Ala Pro Thr Thr Gly Val Val Pro Ala Ala Ala Asp Glu Val Ser
        35                  40                  45
Ala Leu Thr Ala Ala Gln Phe Ala Ala His Ala Gln Met Tyr Gln Thr
    50                  55                  60
Val Ser Ala Gln Ala Ala Ala Ile His Glu Met Phe Val Asn Thr Leu
65                  70                  75                  80
Val Ala Ser Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala Ala
                85                  90                  95
Ala Ala Gly
```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```
Asp Pro His Ala Met Arg Asp Met Ala Gly Arg Phe Glu Val His
1               5                  10                  15
```

(3) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Arg Asp Met Ala Gly Arg Phe Glu Val His Ala Gln Thr Val Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Arg Phe Glu Val His Ala Gln Thr Val Glu Asp Glu Ala Arg Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ala Gln Thr Val Glu Asp Glu Ala Arg Arg Met Trp Ala Ser Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Asp Glu Ala Arg Arg Met Trp Ala Ser Ala Gln Asn Ile Ser Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Trp Ala Ser Ala Gln Asn Ile Ser Gly Ala Gly Trp Ser Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Gln Asn Ile Ser Gly Ala Gly Trp Ser Gly Met Ala Glu Ala Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ala Gly Trp Ser Gly Met Ala Glu Ala Thr Ser Leu Asp Thr Met Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```
Met Ala Glu Ala Thr Ser Leu Asp Thr Met Ala Gln Met Asn Gln
1               5                   10                  15

(2) INFORMATION FOR SEQ ID NO:43:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 15 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: peptide

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ser Leu Asp Thr Met Ala Gln Met Asn Gln Ala Phe Arg Asn Ile
1               5                   10                  15

(2) INFORMATION FOR SEQ ID NO:44:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 15 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: peptide

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ala Gln Met Asn Gln Ala Phe Arg Asn Ile Val Asn Met Leu His
1               5                   10                  15

(2) INFORMATION FOR SEQ ID NO:45:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 18 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: peptide

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ala Phe Arg Asn Ile Val Asn Met Leu His Gly Val Arg Asp Gly
1               5                   10                  15

(2) INFORMATION FOR SEQ ID NO:46:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 15 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: peptide
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Val Asn Met Leu His Gly Val Arg Asp Gly Leu Val Arg Asp Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Gly Val Arg Asp Gly Leu Val Arg Asp Ala Asn Asn Tyr Glu Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Leu Val Arg Asp Ala Asn Asn Tyr Glu Gln Gln Glu Gln Ala Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Asn Asn Tyr Glu Gln Gln Glu Gln Ala Ser Gln Gln Ile Leu Ser Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Ala Ser Arg Phe Met Thr Asp Pro His Ala Met Arg Asp Met Ala
1 5 10 15
Gly

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Asp Ala His Gly Ala Met Ile Arg Ala Gln Ala Ala Ser Leu Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Ile Arg Ala Gln Ala Ala Ser Leu Glu Ala Glu His Gln Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala Glu His Gln Ala Ile Val Arg Asp Val Leu Ala Ala Gly Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ile Val Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu Phe Ile Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Gly Ser Val Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu
1 5 10 15
Gln Ala

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala Asn Ala His Gly Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ile Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln Thr Asp Ser Ala

1 5 10 15

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Gly Asn Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Asp Ala His Gly Ala Met Ile Arg Ala Leu Ala Gly Leu Leu Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Asp Ala His Gly Ala Met Ile Arg Ala Gln Ala Gly Leu Leu Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Ile Arg Ala Gln Ala Gly Leu Leu Glu Ala Glu His Gln Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile Ser Asp Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile Arg Asp Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Ala Glu His Gln Ala Ile Ile Ser Asp Val Leu Thr Ala Ser Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ala Glu His Gln Ala Ile Ile Arg Asp Val Leu Thr Ala Ser Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ile Ile Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ile Ile Arg Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala Ala Cys Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Phe Trp Gly Gly Ala Gly Ser Ala Ala Cys Gln Gly Phe Ile Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Gly Ser Ala Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Val Thr Thr Asn Phe Phe Gly Val Asn Thr Ile Pro Ile Ala Leu Asn
1 5 10 15
Glu Ala Asp Tyr Leu Arg Met Trp Ile
20 25

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Asn Glu Ala Asp Tyr Leu Arg Met Trp Ile Gln Ala Ala Thr Val Met
1 5 10 15
Ser His Tyr Gln Ala Val Ala His Glu
20 25

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 967 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TGAGCGCCAA CCCTACCGTC GGTTCGTCAC ACGGACCGCA TGGCCTGCTC CGCGGACTGC 60
CGCTAGGGTC GCGGATCACT CGGCGTAGCG GCGCCTTTGC CCACCGATAT GGGTTCCGTC 120
ACAGTGTGGT TGCCCGCCCG CCATCGGCCG GATAACGCCA TGACCTCAGC TCGGCAGAAA 180
TGACAATGCT CCCAAAGGCG TGAGCACCCG AAGACAACTA AGCAGGAGAT CGCATGCCGT 240
TTGTGACTAC CCAACCAGAA GCACTGGCGG CGGCGGCCGG CAGTCTGCAG GGAATCGGCT 300
CGGCATTGAA CGCCCAGAAT GCGGCTGCGG CGACTCCCAC GACGGGGTG GTCCGGCGGC 360
CGCCGATGAA NTGTCGGCGC TGACGGCGGC TCAGTTCGCG GCACACGCCC AGATCTATCA 420
GGCCGTCAGC GCCCAGGCCG CGGCGATTCA CGAGATGTTC GTCAACACTC TACAGATGAG 480
CTCAGGGTCG TATGCTGCTA CCGACGCCGC CAACGCGGCC GCGGCCGGNT AGAGGAGTCA 540
CTGCGATGGA TTTTGGGGCG TTCCCGCCGG AGGTCAATTC GGTGCGGATG TATGCCGTTC 600
CTGGCTCGGC ACCAATGGTC GCTGCGGCGT CGGCCTGGAA CGGGTTGGCC GCGGAGCTGA 660
GTTCGGCGGC CACCGGTTAT GAGACGGTGA TCACTCAGCT CAGCAGTGAG GGGTGGCTAG 720
GTCCGGCGTC AGCGGCGATG GCCGAGGCAG TTGCGCCGTA TGTGGCGTGG ATGAGTGCCG 780
CTGCGGCGCA AGCCGAGCAG GCGGCCACAC AGGCCAGGGC CGCCGCGGCC GCTTTTGAGG 840
CGGCGTTTGC CGCGACGGTG CCTCCGCCGT TGATCGCGGC CAACCGGGCT TCGTTGATGC 900
AGCTGATCTC GACGAATGTC TTTGGTCAGA ACACCTCGGC GATCGCGGCC GCGGAAGCTC 960
AGTACGG 967

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Met Ser Phe Val Thr Thr Gln Pro Glu Ala Leu Ala Ala Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Thr Gln Pro Glu Ala Leu Ala Ala Ala Ala Asn Leu Gln Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Leu Ala Ala Ala Ala Ala Asn Leu Gln Gly Ile Gly Thr Thr Met
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Ala Asn Leu Gln Gly Ile Gly Thr Thr Met Asn Ala Gln Asn Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Ile Gly Thr Thr Met Asn Ala Gln Asn Ala Ala Ala Ala Ala Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Asn Ala Gln Asn Ala Ala Ala Ala Ala Pro Thr Thr Gly Val Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Ala Ala Ala Ala Pro Thr Thr Gly Val Val Pro Ala Ala Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Thr Thr Gly Val Val Pro Ala Ala Ala Asp Glu Val Ser Ala Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Pro Ala Ala Ala Asp Glu Val Ser Ala Leu Thr Ala Ala Gln Phe
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Glu Val Ser Ala Leu Thr Ala Ala Gln Phe Ala Ala His Ala Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Thr Ala Ala Gln Phe Ala Ala His Ala Gln Met Tyr Gln Thr Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Ala Ala His Ala Gln Met Tyr Gln Thr Val Ser Ala Gln Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Met Tyr Gln Thr Val Ser Ala Gln Ala Ala Ala Ile His Glu Met Phe
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Ser Ala Gln Ala Ala Ala Ile His Glu Met Phe Val Asn Thr Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ala Ile His Glu Met Phe Val Asn Thr Leu Val Ala Ser Ser Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Phe Val Asn Thr Leu Val Ala Ser Ser Gly Ser Tyr Ala Ala Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Val Ala Ser Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala Ala Ala Ala Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1784 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

ATTCGTTCCT GCCGCAGCTA AATCCCGGGG ACATCGTCGC CGGCCAGTAC GAGGTCAAAG 60
GCTGCATCGC GCACGGCGGA CTGGGCTGGA TCTACCTCGC TCTCGACCGC AATGTCAACG 120
GCCGTCCGGT GGTGCTCAAG GGCCTGGTGC ATTCCGGTGA TGCCGAAGCG CAGGCAATGG 180
CGATGGCCGA ACGCCAGTTC CTGGCCGAGG TGGTGCACCC GTCGATCGTG CAGATCTTCA 240
ACTTTGTCGA GCACACCGAC ACGCACGGGG ATCCGGTCGG CTACATCGTG ATGGAATACG 300
TCGGCGGGCA ATCGCTCAAA CGCAGCAAGG GTCAAAAACT GCCCGTCGCG GAGGCCATCG 360
CCTACCTGCT GGAGATCCTG CCGGCGCTGA GCTACCTGCA TTCCATCGGC TTGGTCTACA 420

ACGACCTGAA GCCCGAAAAC ATCATGCTGA CCGAGGAACA GCTCAAGCTG ATCGACCTGG 480
GCGCCGTATC GCCGATCAAC TCGTTCGGCT ACCTCTACGG GACCCCAGGC TTCCAGGCGC 540
CCGAGATCGT GCCGACCGGT CCGACGGTGG CCACCGACAT CTACACCGTG GGACGCACGC 600
TCGCCGGCGT CACGCTGGAC CTGCCCACCC GCAATGGCCG TTATGTGGAT GGGCTACCCG 660
AAGACGACCC GGTGCTGAAA ACCTACGACT CTTACCGCCG GTTGCTGCGC AGGGCCATCG 720
ACCCCGATCC GCGGCAACGG TTCACCACCG CCGAAGAGAT GTCCGCGCAA TTGACGGCCG 780
TGTTGCGGGA GGTGGTCGCC CAGACACCGG GGTGCCGCGG CCAGGCTATC AACGATCTTC 840
AGTCCCAGTC GGTCGACATT TGGAGTGGAC TGCTGGTGGC GCACACCGAC GTGTATCTGG 900
ACGGCAGGT GCACGCCGAG AAGCTGACCG CCAACGAGAT CGTGACCGCG CTGTCGGTGC 960
CGCTGGTCGA TCCGACCGAC GTCGCAGCTT CGGTCCTGCA GGCCACGGTG CTCTCCCAGC 1020
CGGTGCAGAC CCTAGACTCG NTGCGCGCGG CCCGCCACGG TGCGCTGGAC GCCGACGGCG 1080
TCGATTNTCC GAGTCAGTGG AGCTGCCGCT AATGGAAGTC CGCGCGCTGC TGGATCTCGG 1140
CGATGTGGCC AAGGCCACCC GAAAACTCGA CGATCTGGCC GAACCGGTTG GCTGGCGATG 1200
GCGATTGGTC TGGTACCGGG CCGTCGCCGA GCTGCTCACC GGCGACTATG ACTCGGCCAC 1260
CAAACATTTC ACCGAGGTGC TGGATACCTT TCCCGGCGAG CTGGCGCCCA AGCTCGCCCT 1320
GGCCGCCACC GCCGAACTAG CCGGCAACAC CGACGAACAC AAGTTCTATC AGACGGTGTG 1380
GAGCACCAAC GACGGCGTGA TCTCGGCGGC TTTCGGACTG GCCAGACCCC GGTCGGCCGA 1440
AGGTGATCGG GTCGGCGCCG TGCGCACGCT CGACGAGGTA CCGCCCACTT CTCGGCATTT 1500
CACCACGGCA CGGCTGACCA GCGCGGTGAC TCTGTTGTCC GGCCGGTCAA CGAGTGAAGT 1560
CACCGAGGAA CAGATCCGCG ACGCCGCCCG AAGAGTGGAG GCGCTGCCCC CGACCGAACC 1620
ACGCGTGCTG CAGATCCGCG CCCTGGTGCT GGGTGGCCGC CTGGACTGGC TGAAGGACAA 1680
CAAGGCCAGC ACCAACCACA TCCTCGGTTT CCCGTTCACC AGTCACGGGC TGCGGCTGGG 1740
TGTCGAGGCG TCACTGCGCA GCCTGGCCCG GGTAGCTCCC ACTC 1784

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 766 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ACAARACACT CGGYGGCRGC CSNTCCGGCC TGATCGTCGG TGATCAGCYT CGTGCCAAAY 60
TCGGCACAAG GTGCGCGCTR CCCAANGAGT TCTTCGCCGC RGTGCGNGCN KAACTGGCCT 120
ATCNTGGTTG GGTGCCGTCC CGCANAACCC GCNAACTTAA ACCCATTTTA ACCGGGCAGG 180
AAGTTTCCTA CATYTACCCN RGSMANCCAA CCGGGCCGCC NANAAMTCCG TCCTGGANTC 240
CGANCGGTTC CCGGTGTTCG CCGCACTGCT GACCGGCACG GARTATCCGC AGGCGGCGTT 300
GGCCAACGCG TGGGTGCAAC TGGCCTACGG TGCGCACCAS GACGCCATCA CCGGCTCGGA 360
GTCCGACCAG GTACTCAATG CTGGCGACCA CACCAGCCAG CAGACCAAAC TGGTGCACGC 420
CGATCTCCAG GCGCGCCGGC CCGGTGGCAT ACCGATTGGT CGAAACCAAT CCGAAGGAAT 480
TCATCACGGA CGGTCACGGA AAACGATCGC CCCAATGGGN GGACNACCCN AGCCAGGCGN 540
ATTNACCGTT NAACAAGTTG GNGTAGGTTC TTTGATATCG ANCAACCGAT ACGGARCGGN 600
CCGCGGAATG GTAGACCACC ACCAGTGCCC NCAMGTNGTG CACCAGTTTG GTCATCGCCC 660
GCAGATCGGT GACCCCGCCA AGCGTTCCGG ATGCGGAGAT GASGGTGACC AGCCYGGTTG 720
ACCTGTTGAT CAGGTTNTCC CAGTGCCACG TCGGCAGCTG GCCGGT 766

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```
CGGCACGAGA ATGTCGCCTG TGCCTCGATA GCCACTTGCG TGTGGTCGCG CTGCCAGCGG     60
GTCAGCCAGG TCGCCTGGTC CAGGCCATCG GGCCGGCGCA GGAGCGCGAT GTTGGCCAGA    120
CCCGGTGTAC GAGAACCGGA CTCGACNAAG TGTCGGCGCT GACGGCGGCT CAGTTCGCGG    180
CACACGCCCA GATCTATCAG GCCGTCAGCG CCCAGGCCGC GGCGATTCAC GAGATGTTCG    240
TCAACACTCT ACAGATNANC TCAGGGTCGT ATGCTGCTAC CGAGGCCGCC AACGCGGCCG    300
CGGCCGGCTA GAGGAGTCAC TGCGATGGAT TTTGGGGCGT TGCCGCCCGA GGTCAATTCG    360
GTGCGGATGT ATGCCGGTCC TGGCTCGGCA CCAATGGTCG CTGCGGCGTC GGCCTGGAAC    420
GGGTTGGCCG CNGAGCTGAG TTCGGCGGCC ACCGGTTATG AGACGGTGAT CACTCAGCTC    480
AGCAGTGAGG GGTGGCTAGG TCCGGCGTCA GCGGCGATGG CCGAGGCAGT TGCGCCGTAT    540
GTGGCGTGGA TGAGTGCCGC TGCGGCGCAA GCCGAGCAGG CGGCCACACA GGCCAGGGCC    600
GCCGCGGCCG CTTTTGAGGC GGCGTTTGCC GCGACGGTGC CTCCGCCGTT GATCGCGGCC    660
AACCGGGCTT CGTTGATGCA GCTGATCTCG ACGAATGTCT TTGGTCAGAA CACCTCGGCG    720
ATCGCGGCCG CCGAAGCTCA GTACGGCGAG ATGTGGGCCC AAGACTCCGC GGCGATGTAT    780
GCCTACGCGG GCAGTTCGGC GAGCGCCTCG GCGGTCACGC CGTTTAGCAC GCCGCCGCAG    840
ATTGCCAACC CGACCGCTCA GGGTACGCAG GCCGCGGCCG TGGCCACCGC CGCCGGTACC    900
GCCCAGTCGA CGCTGACGGA GATGATCACC GGGCTACCCA ACGCGCTGCA AAGCCTCACC    960
TCACNTCTGT TGCAGTCGTC TAACGGTCCG CTGTCGTGGC TGTGGCAGAT CTTGTTCGGC   1020
ACGCCCAATT TCCCCACCTC AATTTCGGCA CTGCTGACCG ACCTGCAGCC CTACGCGAGC   1080
TTNTTNTATA ACACCGAGGG CCTGCCGTAC TTCAGCATCG GCATGGGCAA CAACTTCATT   1140
CAGTCGGCCA AGACCCTGGG ATTGATCGGC TAGGCGGCAC CGGCTGCGGT CGCGGNTGCT   1200
GGGGATNCCG CCAAGGGCTT GCCTCGTGCC G                                  1231
```

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2041 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```
CGGCACGAGC TCGTGCCGAT CAGTGCCATT GACGGCTTGT ACGACCTTCT GCGGGATTGGA     60
ATACCCAACC AAGGGGGTAT CCTTTACTCC TCACTAGAGT ACTTCGAAAA AGCCCTGGAG    120
GAGCTGGCAG CAGCGTTTCC GGGTGATGGC TGGTTAGGTT CGGCCGCGGA CAAATACGCC    180
GGCAAAAACC GCAACCACGT GAATTTTTTC CAGGAACTGG CAGACCTCGA TCGTCAGCTC    240
ATCAGCCTGA TCCACGACCA GGCCAAGCGC GTCCAGACGA CCCGCGACAT CCTGGAGGGC    300
GCCAAGAAAG GTCTCGAGTT CGTGCGCCCG GTGGCTGTGG ACCTGACCTA CATCCCGGTC    360
GTCGGGCACG CCCTATCGGC CGCCTTCCAN GCGCCGTTTT GCGCGGGCGC GATGGCCGTA    420
GTGGCCGGCG CGCTTGCCTA CTTGGTCGTG AAAACGCTGA TCAACGCGAC TCAACTCCTC    480
AAATTGCTTG CCAAATTGGC GGAGTTGGTC GCGGCCGCCA TTGCGGACAT CATTTCGGAT    540
GTGGCGGACA TCATCAAGGG CATCCTCGGA GAAGTGTGGG AGTTCATCAC AAACGCGCTC    600
AACGGCCTGA AAGAGCTTTG GGACAAGCTC ACGGGGTGGG TGACCGGACT GTTCTCTCGA    660
GGGTGGTCGA ACCTGGAGTC CTTCTTTGCG GGCGTCCCCG GCTTGACCGG CGCGACCAGC    720
GGCTTGTCGC AAGTGACTGG CTTGTTCGGT GCGGCCGGTC TGTCCGCATC GTCGGGCTTG    780
GCTCACGGCG ATAGCCTGGC GAGCTCAGCC AGCTTGCCCG CCCTGGCCGG CATTGGGGGC    840
GGGTCCGGTT TTGGGGGCTT GCCGAGCCTG GCTCAGGTCC ATGCCGCCTC AACTCGGCAG    900
GCGCTACGGC CCCGAGCTGA TGGCCGGGTC GGCGCCGCTG CCGAGCAGGT CGGCGGGCAG    960
TCGCAGCTGG TCTCCGCGCA GGGTTCCCAA GGTATGGGCG GACCCGTAGG CATGGGCGGC   1020
ATGCACCCCT CTTCGGGGGC GTCGAAAGGG ACGACGACGA AGAAGTACTC GGAAGGCGCG   1080
GCGGCGGGCA CTGAAGACGC CGAGCGCGCG CCAGTCGAAG CTGACGCGGG CGGTGGGCAA   1140
AAGGTGCTGG TACGAAACGT CGTCTAACGG CATGGCGAGC CAAATCCATT GCTAGCCAGC   1200
```

GCCTAACAAC GCGCAATGCT AAACCGAAGG GACACGATCA ATGACGGAAA ACTTGACCGT 1260
CCAGCCCGAG CGTCTCGGTG TACTGGCGTC GCACCATGAC AACGCCGCGG TCGATGCGTC 1320
CTCGGGCGTC GAAGCTGCCG CTGGCCTAGG CGAATCTGTG GCGATCACTC ACGGTCGGTA 1380
CTGCTCACAG TTCAACGACA CGTTAAATGT GTACTTGACT GCCCACAATG CCCTGGGCTC 1440
GTCCTTGCAT ACGGCCGGTG TCGATCTCGC CAAAAGTCTT CGAATTGCGG CGAAGATATA 1500
TAGCGAGGCC GACGAAGCGT GGCGCAAGGC TATCGACGGG TTGTTTACCT GACCACGTTT 1560
GCTGCCCGCA GTGCAGGCCA CGACGTAGCG CAGGTCGTGT CCCTCGTAGG CGTGGATGCG 1620
ACCGGCCAGC ACCAGCACCC GGTGCGCACC GATGGGCACG GACAGTAGCT CGCCCGCATG 1680
CCCGGCTGCG GTTGGCGGCA CAAACCCGGG CAGTTCGGCC TGCCGCAGCA CGGTGGTGGG 1740
GGAGCCCAAC GCCGCAACGG CCGGTAACCA TCCCGACCCG AGCACGACCG AGACGTCATG 1800
TTCGCCGATC CCGGTGCGGT CAGCGATGAC CTGCGCCGCC CGCCGGGCCA GTTTGTCGGG 1860
ATCGGGGCGC GGGTCAGCCA CACTGGGCGA GCTTAACTGA GCCGCTCGCC GGGGAGCGGG 1920
TGCTNGTCGA TGAGATACTG CGAGCATGCC AGCAGCCAGC GCATCCGACC GCGTCGAGGA 1980
ATTGGTGCGG CGCCGTGGTG GCGAGCTGGT CGAGCTGTCC CATGCCATCC ACCTCGTGCC 2040
G 2041

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GAGCTCACCG CTATCAACCA ATACTTTCTG CACTCCAAGA TGCAGGACAA CTGGGGTTTT 60
ACCGAGCTGG CGGCCCACAC CCGCCGCGAG TCGTTCGACG AAATGCCGCA CGCCGAGGAA 120
ATCACCGATC GCATCTTGTT GCTGGATGGT TTGCCGAACT ACCAGCGCAT CGGTTCGTTG 180
CGTATCGGCC AGACGCTCCG CGAGCAATTT GAGGCCGATC TGGCGATCGA ATACGACGTG 240
TTGAATCGTC TCAAGCCAGG AATCGTCATG TGCCGGGAGA AACAGGACAC CACCAGCGCC 300
GTACTGCTGG AGAAAATCGT TGCCGACGAG GAAGAACACA TCGACTACTT GGAAACGCAG 360
CTGGAGCTGA TGGACAAGCT AGGAGAGGAG CTTTACTCGG CGCAGTGCGT CTCTCGCCCA 420
CCGACCTGAT GCCCGCTTGA GGATTCTCCG ATACCACTCC GGGCGCCGCT GACAAGCTCT 480
AGCATGGACT CGAACAGCGA TGGGAGGGCG GATATGGCGG GCCCCACAGC ACCGACCACT 540
GCCCCCACCG CAATCCGAGC CGGTGGCCCG CTGCTCAGTC CGGTGCGACG CAACATTATT 600
TTCACCGCAC TTGTGTTCGG GGTGCTGGTC GCTGCGACCG GCCAAACCAT CGTTGTGCCC 660
GCATTGCCGA CGATCGTCGC CGAGCTGGGC AGCACCGTTG ACCAGTCGTG GGCGGTCACC 720
AGCTATCTGC TGGGGGGAAC ACTSICYGKKK KTGKKGKSYS KSRMRMKCTC GGTGATCTGC 780
TCGGCCGCAA CAGGCTGCTG CTAGGCTCCG TCGTGGTCTT CGTCGTTGGC TCTGTGCTGT 840
GCGGGTTATC GCAGACGATG ACCATGCTGG CGATCTCTCG CGCACTGCAG GGCGTCGGTG 900
CCGGTGCGAT TTCCGTCACC GCCTACGCGC TGGCCGCTGA GGTGGTCCCA CTGCGGGACC 960
GTGCCCGCTA CCAGGGCGTC TTANGTGCGG TGTTCGGTGT CAACACGGTC ACCGGTCCGC 1020
TGCTGGGGGG CTGGCTCACC GACTATCTGA GCTGGCGGTG GGCGTTCCGA CCACCAGCCC 1080
CATCACCGAC CCGATCGCGG TCATCGCGGC GAACACCGCC CTCGCGGCGT TGCGGGCAGG 1140
TCCCTTGGGG AACGTGGTCC CACAGCGCCA GAACGGTCGG AAATGCGATG GCCGACCCAC 1200
AC 1202

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 496 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```
GGCGGCGGCA GTTGGCCAGC AGTTNGGGCG GGGGAGCCGG TTCGGNGACC AAGAAATCGG      60
CCTGGGCAAG CAGCCGGGAC CGCGNACCGT GATCAGTTNG GATCGCCGGG ACCGCCGCCG     120
ACCAANGCCA TTCCGCCGNT GAGGAAGTCG GAANTNTGCG CAGTGATGAC GCCCTGCTGC     180
AACGCNTCCC GGATTGCCGA GCGGATCGCC GCCGAACGGC GGTGCTCACC ACCGGCGAGC     240
ACCCCTACNG ACAGGCCCGC ATAGCTGAAT GACGCCGGGT NACCGCCGTC CCNTCCACCG     300
NGANATCGGC CCGGANGCAA AAGATCCGTC GGCGCTCCGC CTCGGCGACG ACAGCCACGT     360
TCACCCGCGC GTTATCGGTG GCCGCGATCG CATACCAGGC GCCGTCAAGG TNGCCGTYGC     420
GGTAGTCACG CACCGACAAG GTGATYTGGT CCATCGCCTN GRCGGCGGGG GTGACGCTGG     480
CGGCGATCAM GTGCAC                                                     496
```

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 849 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```
TGGATTCCGA TAGCGGTTTC GGCCCCTCGA CGGGCGACCA CGGCGCGCAG GCCTCCGAAC      60
GGGGGGCCGG GACGCTGGGA TTCGCCGGGA CCGCAACCAA AGAACGCCGG GTCCGGGCGG     120
TCGGGCTGAC CGCACTGGCC GGTGATGAGT TCGGCAACGG CCCCCCGATG CCGATGGTGC     180
CGGGGACCTG GGAGCAGGGC AGCAACGAGC CCGAGGCGCC CGACGGATCG GGGAGAGGGG     240
GAGGCGACGG CTTACCGCAC GACAGCAAGT AACCGAATTC CGAATCACGT GGACCCGTAC     300
GGGTCGAAAG GAGAGATGTT ATGAGCCTTT TGGATGCTCA TATCCCACAG TTGGTGGCCT     360
CCCAGTCGGC GTTTGCCGCC AAGGCGGGGC TGATGCGGCA CACGATCGGT CAGGCCGAGC     420
AGGCGGCGAT GTCGGCTCAG GCGTTTCACC AGGGGGAGTC GTCGGCGGCG TTTCAGGCCG     480
CCCATGCCCG GTTTGTGGCG GCGCCGCCA AAGTCAACAC CTTGTTGGAT GTCGCGCAGG     540
CGAATCTGGG TGAGGCCGCC GGTACCTATG TGGCCGCCGA TGCTGCGGCC GCGTCGACCT     600
ATACCGGGTT CTGATCGAAC CCTGCTGACC GAGAGGACTT GTGATGTCGC AAATCATGTA     660
CAACTACCCC GCGATGTTGG GTCACGCCGG GGATATGGCC GGATATGCCG GCACGCTGCA     720
GAGCTTGGGT GCCGAGATCG CCGTGGAGCA GGCCGCGTTG CAGAGTGCGT GGCAGGGCGA     780
TACCGGGATC ACGTATCAGG CGTGGCAGGC ACANTGGTAA CCAMGCCANG GAAGATTTGG     840
TGCGGCCT                                                             849
```

(3) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```
Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
 1               5                  10                  15
Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
            20                  25                  30
```

```
Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
        35                  40                  45
Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys
    50                  55                  60
Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
65                  70                  75                  80
Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly
                85                  90                  95
Phe
```

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

```
Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln
 1               5                  10                  15
```

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

```
Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
 1               5                  10                  15
```

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```
Leu Val Ala Ser Gln Ser Ala Phe Ala Ala Lys Ala Gly Leu Met
 1               5                  10                  15
```

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Ser Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala Met Ser Ala Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Gln Ala Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln Ala Ala His
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Glu Ser Ser Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala Arg Phe Val Ala Ala Ala Ala Lys Val Asn Thr Leu Leu Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala Ala Ala Lys Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

```
Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val Ala Ala
 1               5                  10                  15
Asp Ala
```

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1752 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

```
CGGCACGAGA ATGTCGCCTG TGCCTCGATA GCCACTTGCG TGTGGTCGCG CTGCCAGCGG      60
GTCAGCCAGG TCGCCTGGTC CAGGCCATCG GGCCGGCGCA GGAGCGCGAT GTTGGCCAGA     120
CCCGGTGTAC GAGAACCGGA CTCGACNAAG TGTCGGCGCT GACGGCGGCT CAGTTCGCGG     180
CACACGCCCA GATCTATCAG GCCGTCAGCG CCCAGGCCGC GGCGATTCAC GAGATGTTCG     240
TCAACACTCT ACAGATNANC TCAGGGTCGT ATGCTGCTAC CGAGGCCGCC AACGCGGCCG     300
CGGCCGGCTN GAGGAGTCAC TGCGATGGAT TTTGGGGCGT TGCCGCCGGA GGTCAATTCG     360
GTGCGGATGT ATGCCGGTCC TGGCTCGGCA CCAATGGTCG CTGCGGCGTC GGCCTGGAAC     420
GGGTTGGCCG CGGAGCTGAG TTCGGCGGCC ACCGGTTATG AGACGGTGAT CACTCAGCTC     480
AGCAGTGAGG GGTGGCTAGG TCCGGCGTCA GCGGCGATGC CCGAGGCAGT TGCGCCGTAT     540
GTGGCGTGGA TGAGTGCCGC TGCGGCGCAA GCCGAGCAGG CGGCCACACA GGCCAGGGCC     600
GCCGCGGCCG CTTTTGAGGC GGCGTTTGCC GCGACGGTGC CTCCGCCGTT GATCGCGGCC     660
AACCGGGCTT CGTTGATGCA GCTGATCTCG ACGAATGTCT TTGGTCAGAA CACCTCGGCG     720
ATCGCGGCCG CCGAAGCTCA GTACGGCGAG ATGTNGGCCC AAGACTCCGC GGCGATGTAT     780
GCCTACGCGG GCAGTTCGGC GACGCCCTCG GCGGTCACGC CGTTTAGCAC GCCGCCGCAG     840
ATTGCCAACC CGACCGCTCA GGGTACGCAG GCCGCGGCCG TGGCCACCGC CGCCGGTACC     900
GCCCAGTCGA CGCTGACGGA GATGATCACC GGGCTACCCA ACGCGCTGCA AAGCCTCACC     960
TCACNTCTGT TGCAGTCGTC TAACGGTCCG CTGTCGTGGC TGTGGCAGAT CTTGTTCGGC    1020
ACGCCCAATT TCCCCAGCTC AATTTCGGCA CTGCTGACCG ACCTGCAGCC CTACGCGAGC    1080
TTNTTNTATA ACACCGAGGG CCTGCCGTAC TTCAGCATCG GCATGGGCAA CAACTTCATT    1140
CAGTCGGCCA AGACCCTGGG ATTGATCGGC TAGGCGGCAC CGGCTGCCGT CGCGGCTGCT    1200
GGGGATGCCG CCAAGGGCTT GCCTGGACTG GGCGGGATGC TCGGTGGCGG GCCGGTGGCG    1260
GCGGGTCTGG GCAATGCGGC TTCGGTTGGC AAGCTGTCGG TGCCGCCGGT GTGGANTGGA    1320
CCGTTGCCCG GGTCGGTGAC TCCGGGGGCT GCTCCGCTAC CGGTGACTAC GGTCAGTGCC    1380
GCCCCGGAGG CGGCGCCCGG AAGCCTGTTG GGCGGCCTGC CGCTANCTGG TGCGGGCGGG    1440
GCCGGCGCGG GTCCACGCTA CGGATTCCRT CCCACCGTCA TGGCTCGCCC ACCCTTCGMC    1500
GGGATAGTCG CTGCCGCAAC GTATTAACGC GCCGGCCTCG GCTGGTGTGG TCCGCTGCGG    1560
GTGGCAATTG GTCNGCGCCG AAATCTCGGT GGGTTATTTR CGGTGGGATT TTTTCCCGAA    1620
GCCGGGTTCA RCACCGGATT TCCTAACGGT CCCGCKACTC TCGTGCCGAA TTCSGCACTA    1680
AGTGACGTCC GGCGGAAACC CGTTGGGTNT GAAAGCTTCA GAAAGGCCCG CTCCCAGGGG    1740
TTCGGCAAAC GG                                                        1752
```

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

```
Met Asp Phe Gly Ala Leu Pro Pro Glu Val Asn Ser Val Arg Met Tyr
 1               5                  10                  15
Ala Gly Pro Gly Ser Ala Pro Met Val Ala Ala Ala Ser Ala Trp Asn
            20                  25                  30
Gly Leu Ala Ala Glu Leu Ser Ser Ala Ala Thr Gly Tyr Glu Thr Val
        35                  40                  45
Ile Thr Gln Leu Ser Ser Glu Gly Trp Leu Gly Pro Ala Ser Ala Ala
    50                  55                  60
Met Ala Glu Ala Val Ala Pro Tyr Val Ala Trp Met Ser Ala Ala Ala
65                  70                  75                  80
Ala Gln Ala Glu Gln Ala Ala Thr Gln Ala Arg Ala Ala Ala Ala Ala
                85                  90                  95
Phe Glu Ala Ala Phe Ala Ala Thr Val Pro Pro Pro Leu Ile Ala Ala
            100                 105                 110
Asn Arg Ala Ser Leu Met Gln Leu Ile Ser Thr Asn Val Phe Gly Gln
        115                 120                 125
Asn Thr Ser Ala Ile Ala Ala Ala Glu Ala Gln Tyr Gly Glu Met Trp
    130                 135                 140
Ala Gln Asp Ser Ala Ala Met Tyr Ala Tyr Ala Gly Ser Ser Ala Ser
145                 150                 155                 160
Ala Ser Ala Val Thr Pro Phe Ser Thr Pro Pro Gln Ile Ala Asn Pro
                165                 170                 175
Thr Ala Gln Gly Thr Gln Ala Ala Ala Val Ala Thr Ala Ala Gly Thr
            180                 185                 190
Ala Gln Ser Thr Leu Thr Glu Met Ile Thr Gly Leu Pro Asn Ala Leu
        195                 200                 205
Gln Ser Leu Thr Ser Xaa Leu Leu Gln Ser Ser Asn Gly Pro Leu Ser
    210                 215                 220
Trp Leu Trp Gln Ile Leu Phe Gly Thr Pro Asn Phe Pro Thr Ser Ile
225                 230                 235                 240
Ser Ala Leu Leu Thr Asp Leu Gln Pro Tyr Ala Ser Xaa Xaa Tyr Asn
                245                 250                 255
Thr Glu Gly Leu Pro Tyr Phe Ser Ile Gly Met Gly Asn Asn Phe Ile
            260                 265                 270
Gln Ser Ala Lys Thr Leu Gly Leu Ile Gly Ser Ala Ala Pro Ala Ala
        275                 280                 285
Val Ala Ala Ala Gly Asp Ala Ala Lys Gly Leu Pro Gly Leu Gly Gly
    290                 295                 300
Met Leu Gly Gly Gly Pro Val Ala Ala Gly Leu Gly Asn Ala Ala Ser
305                 310                 315                 320
Val Gly Lys Leu Ser Val Pro Pro Val Trp Xaa Gly Pro Leu Pro Gly
                325                 330                 335
Ser Val Thr Pro Gly Ala Ala Pro Leu Pro Val Ser Thr Val Ser Ala
            340                 345                 350
Ala Pro Glu Ala Ala Pro Gly Ser Leu Leu Gly Gly Leu Pro Leu Xaa
        355                 360                 365
Gly Ala Gly Gly Ala Gly Ala Gly Pro Arg Tyr Gly Phe Xaa Pro Thr
    370                 375                 380
Val Met Ala Arg Pro Pro Phe Xaa Gly Ile Val Ala Ala Ala Thr Tyr
385                 390                 395                 400
```

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 474 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GGCACGAGCA CCAGTTGACC CGCGAAGAAC CTGACCGCGC CACCCAGCGC CGCCCGCATC 60
ACCGGCCCCG TCCCACGAAC CTTTTCGGTA AACGAGCCAC TCCAGCGGAG ATCGGTACCG 120
CCCGACGCAT TTGGTGTAAG GACCACCTCG CCGAAGTAGT CCTGGACGGG TGTCCTCGCG 180
CCAACCAGCT TGTAGACGTG GCGACGGTCC TGCTCATACT CGACGGTCTC TTCCTGCACG 240
AACACCGGCC ACATGCCTAG TTTGCCGATG GCCCCGATGC CGCCGGGCGC GGGATCACCG 300
CGTCGCGCCC AACTCGATTG AGCAACGATG GGCTTGGCCC AGGTCGCCCA GTTGCCACCG 360
TCTGTCACGA GCCGAAACAA GGTTGCAGCC GGCGCGCTGC TGGTCTTGGT GACCTCGAAC 420
GAAAATTTCC GACCCGACAT GCGCGACTCC CGAAACGACA ACTGAAGCTC GTGC 474

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1431 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CTGCGCGCCG GAAAAAANTA TTACTGGCAG GACCGGCAGA ATGCATGGTG ATATTCCGGT 60
GATGAGGCCG CCGAGGAACC GACTAGTGCG AGGGTCAACA CATCGGTTAT TCGTTGCCGT 120
TTAGGTCTTG GATCTGCCGG GACGGCAACG AGTTGGCAGG ACCGCTCACG CGAGCGCTGT 180
TGACAGAGTC GGTTCACGTC GAACTCGCCA CCCGTCAGAT GCGAATGATA GCCACATCGG 240
CCACACCATC GACGGCGTCG AAGTCGCCGT CGTGGGTCAC GACCGGCACC CCTTGCGACG 300
TGGCAACGGC AGCGGCCCTC ACCGGACGGG ACCGAGATCG TCGGTGGTGT CGCCAGTGAG 360
CGTTGCGAGG TCGCGGGTGC AATCCCGCAT CTGCTTGCGT ATGCCGAAGC CGCCGCAGCA 420
GCTCGTCTCG ACTCAACCAT CGGCGCCGTG CGGGCTGCCT GCGGTCAGCA GCGCAACGGG 480
TTTGCCGTTG GCAGTGATGG TGATGTCTTC GCCGGCCTGC ACGCGCCGTA GCAGCCCGGC 540
GGTGTTGTTG CGCAGTTCGC GAGACGCGAC TTCAGCAGGC ATGCTGCGGG GATCGGCTTG 600
CGCTGGGCGC GGTGTCACCG TCATGCGCTT GGGATATCAC GTGATCTATC GGCACGAAGC 660
CGCCGGATGA GCGAGGCAAA CCGCCTACAC GGGCTGCCTC GCCTTGACCG CGCCGAACGT 720
TACTGTGCCG GGGGCATCAG CACCGTATCG ATCATGTACA CCGTCGCGTG GGCGGTGTGA 780
CTCCGCCACA TACCAAACGG GCGTTGTTGA CCATGAGTCG TCGCUGGCGC CTATCACCGT 840
CAGGTCGGCA CCTTGCAGGT CTGATGGGTG CCGTCGATCC TGCTCGGACT CGCCTGGCCG 900
GCTATCACGT GGTAGGTCAG GATGCTGCTG AGCAGCTTGG CGTCAGTCTT GAGTTGATCG 960
ATAGTGGCCG CCGGCAGCTT GTCGAATGCG GCGTTGGTGG GGGCGAAAAC GGTGTACTCG 1020
CCGCCGTTGA GGGTGTCGAC CAGATTCACA TCCGGGTTCA GCTTGCCCGA CAGAGCCGAG 1080
GTCAGGGTAC TGAGCATCGG GTTGTTGGAA GCCGCGGTAG CGACCGGGTC TTGCGCCATT 1140
CCGGCCACCG ATCCGGGACC GGTGGGATTT TGCGCCGCGT ATTGCGCGCA CCCACGACCA 1200
ATCAGGTCCG CTGCGGTCAG CCATTGCCGC CGTGGTAACG GGCGCCGCCG GGCTGGTCGC 1260
CGGTTTCGGG CTGGTGTCTT GCGACACGGG TTTGGTGCTC GAACAACCCG CTAAGAACGC 1320
AATGCCGATG GCTGCGAGGC TCGCTGCTGC GGCCGGTTTG GCCTGAACGT TGATCATCGC 1380
TTCGATTCCT TTGCTTCTGC GGCGGCGTTG AACGCCGTCC TCCTGGGTGG A 1431

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GCACGAGAGT CGTATCTTTG CACCCAGCGC CCGTAGGAAA CCGCTGGCCT GGCTAACTCA 60
GATGCGGGCG GCCGTCGATT CGAGAGGTAA CCGATCGCCC GCCGACAATG GGTTACCCAC 120
CGAGACTGAT TGCCGCCGCAG CCGCCTTCGA CGTGTAAGCG CCGGTTCGTG CATGCCCGGA 180
ACGGCTGCAC TCACGGACCT TCTACGTAGT ACGTGACGGA CTTTTACGCA TTATCGCTGA 240
CGATCTTTGC CTCCCAGGAC TCCAGAATCT ACTCGTGCC 279

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1470 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

ACCGCCACCC GCAGCCCGGA ATCACCGTCG GTAACCTGCG AATACAATTT CTTCATCGAC 60
GACTTCGCGA ACAGCGAACC CGAGCCCACC GCCTGATAGC CTTCTTCCTC GATGTTCCAA 120
CCGCCGGCGG CGTCGAACGA AACGATACGA CCCGCGCTCT GCGGGTCAGA CGCATGAATG 180
TCGTAGCCCG CCAGCAACGG CAACGCCAGC AGACCCTGCA TCGCGGCCGC CAGATTGCCA 240
CGCACCATAA TCGCCAGCCG GTTGATTTTG CCGGCAAACG TCAGCGGCAC ACCCTCGAGC 300
TTCTCGTAGT GCTCAAGTTC CACGGCATAC AGCCGGGCAA ACTCAACCGC GACCGCAGCC 360
GTGCCAGCGA TGCCGGTAGC GGTGTAGTCA TCGGTGATAT ACACCTTGCG CACATCACGC 420
CCAGAAATCA TGTTGCCCTG CGTCGAACGC CGGTCACCCG CCATGACAAC ACCGCCGGGG 480
TATTTCAGCG CGACAATGGT GGTGCCGTGC GGCAGTTGCG CATCGCCGCC TGCGAGTGGC 540
GCACCGCCGC TGATGCTTGC CGGCAGCAAC TCCGGCGCCT GGCGGCGCAG GAAGTCAAGT 600
GAAAGAAGAT AGGTCTACAG CGGGTGTTCC AGAGAGTGAA TTAATGGACA GGCGATCGGG 660
CAACGGCCAG GTCACTGTCC GCCCTTTTGG ACGTATGCGC GGACGAAGTC CTCGGCGTTC 720
TCCTCGAGGA CGTCGTCGAT TTCGTCGAGC AGATCGTCGG TCTCCTCGGT CAGCTTTTCG 780
CGACGCTCCT GGCCCGCGGC GGTGCTGCCG GCGATGTCGT CATCATCGCC GCCGCCACCG 840
CCACGCTTGG TCTGCTCTTG CGCCATCGCC GCGTCCTGCT TCCTCATGGC CTTTCAAAAG 900
GCCGCGGGTG CGCGTCACAC GCCCGCTGTC TTTCTCTCAC CTACCGGTCA ACACCAACGT 960
TTCCCGGCCT AACCAGGCTT AGCGAGGCTC AGCGGTCAGT TGCTCTACCA GCTCCACGGC 1020
ACTGTCCACC GAATCCAGCA ACGCACCAAC ATCCGCCTTA CTACCCCGCA ACGGCTCCAG 1080
CGTCGGGATG CGAACCAGCG AGTCGCCGCC AGGTCGAAGA TCACCGAGTC CCAGCTAGCC 1140
GCGGCGATAT CAGCCCCGAA CCGGCGCAGG CATTTCGCCG CGGAAATACG CGCGGGTGTC 1200
GGTCGGCGGT TCTCCACCGC ACTCAGCACC TGGTGTTTCG GTGACTAAAC GCTTTATCGA 1260
GCCCCGCGCG ACCAGCCGGT TGTACAGGCC CTTGTCCAGC CGGACATCGG AGTACTGCAG 1320
GTTGACGAGG TGCAGCCGGG GCGCCGACCA GCTCAGGTTC TCCCGCTGCC GGAAACCGTC 1380
GAGCAGCCGC AGTTTGGCCG GCCAGTCCAG CAGCTCCGCG CAATCCATCG GGTCACGCTC 1440
GAGCTGATCC AGCACGTGTG CCCAGGTTTC 1470

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1059 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```
ATTCCCATCG CTCCGGCACC TATCACCAGG TAGTCGGTTT CGATGGTTTT CGCCGGCCCT      60
TGCGTTGGCC TGGGCCACGG GTCGTTCATG GGCCCTCCTG TGCGGATTGG AATTTGTGAC     120
AACGAAATCG GGCGATCGGT GAGCAATCGT CGCCGATGCA AGACACGCTT TCGCTGCCGC     180
GGCGTCAGGT GGAGTTTAGG CCAGCGTAAC AACGTAGACC GGCCACTGAC CAAACCCCAA     240
ACCCACAAAC CCTGGACGCA TGCGGGTCTC GGGCGTCAAA TTCCGGGTAG ATATCGTATA     300
CCGATATCGG ATGCCGTAGC CTTATCGAGG CATGAGACGC CCGCTAGACC CACGCGATAT     360
TCCAGATGAG CTGCCGCGAC GGCTGGGGCT CTTCGATGCG GTGGTGATCG GGCTTGGGTC     420
CATGATCGGT GCCGGAATCT TTGCTCGTGC CGAATTCGGC ACGAGCTCGT GCCGAATTCG     480
GCACGAGATT CCAATCCCCA GAAGGTCGTA CAAGCCGTCA ATGGCACTTG ATCGTTGGAT     540
CGATGATGAA CGCTCTGCTC ATGCCTGCCG CCTATCTCAA CGGTCGTCGA TTCCATGCAT     600
TAGCCTTGGT TCTGCATTGC ACGCGTAGGG CCTACAGTCT GGCTGTCATG CTTGGCCGAT     660
GTCAACAGTT TTTTTCATGC TAAGCAGATC GTCAGTTTTG AGTTCGTGAA GACGGCATGT     720
TCACTTGTTG TCGACTACAT CGTCTGCGCA CATTTGCCCT CCTGCAACTG CGCTGCGACA     780
ATGCGCCAAC CGCCGTGTAG CTCGTGCCGA ATTCGGCACG AGGATCCACC GGAGATGGCC     840
GACGACTACG ACGAGGCCTG GATGCTCAAC ACCGTGTTCG ACTATCACAA CGAGAACGCA     900
AAAGAAGAGG TCATCCATCT CGTGCCCGAC GTGAACAAGG AGAGGGGGCC CATCGAACTC     960
GTAACCAAGG TAGACAAAGA GGGACATCAG ACTCGTCTAC GATGGGGAGC CACGTTTTCA    1020
TACAAGGAAC ATCCTAAGTT TTGATTCGGG AACATCCTA                            1059
```

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```
GCACGAGGCA TTGGCGGGCA TCTGCATAAA CGGTGACGTA TCAGCACAAA ACAGCGGAGA      60
GAACAACATG CGATCAGAAC GTCTCCGGTG GCTGGTAGCC GCAGAAGGTC CGTTCGCCTC     120
GGTGTATTTC GACGACTCGC ACGACTCGTG CCG                                  153
```

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```
CCGCGCGGTC GATCAGCGAG CCAGGCAAAA ACTCCGTCGA GCCCGAGTCG ATGATGGTCA      60
CCCGGCCCAG CATCTGGCGA ACGATCACCT CGATGTGCTT GTCGTGGATC GACACACCTT     120
GGGCGCGGTA GACCTCCTGG ACCTCGCGAA CCAGGTGTAT CTGCACCTCG CGGGGCCCCT     180
GCACCCGCAG CACCTCATGC GGGTCGGCCG AGCCTTCCAT CAGCTGCTGG CCCACCTCGA     240
CGTGGTCGCC ATCGGAGAGC ACCCGTTCGG AACCGTCTTC GTGCTTGAAC ACCCGCAGCC     300
GCTGCCGCTT GGAGATCTTG TCGTAGACCA CTTCCTCACC GCCGTCGTCA GGAACGATGG     360
TGATCTTGTA GAACCGCTCG CCGTCCT                                         387
```

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 389 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GTTCAGCACG GCTATCCGAT TGTGCCGTTC GCTTCGGTGG GTGCTGAACA CGGCATCGAC 60
ATCGTGCTCG ACAACGAATC CCCACTGCTG GCACCGGTCC AGTTCCTCGC CGAGAAGCTG 120
CTCGGCACCA AAGACGGTCC GGCGCTGGTC CGTGGTGTCG GACTGACACC GGTACCGCGC 180
CCCGAACGGC AGTATTACTG GTTCGGCGAG CCAACCGACA CCACAGAGTT TATGGGGCAG 240
CAAGCCGACG ATAACGCCGC ACGCAGGGTG CGCGAGCGTG CCGCCGCCGC TATCGAACAC 300
GGCATCGAGC TGATGCTGGC CGAGCGCGCA GCCGATCCAA ATCGATCCCT GGTCGGACGG 360
CTCTTGCGCT CCGACGCCTA AGCCGCCCC 389

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

CCCGCCGGTCG GAATGATCCC CGTCTCGTCG CGCGCCCATT TGATGCTGTT GATGAGCTGT 60
TTGGAGAAGC CCGGTTGGCG TACCGGTGAG CCGGAATATC TGTTTGGAAGC GTCACCGGAT 120
GTNCACATGA ANTNCNTTGN CCCNGTNGCG GTNTTGGNTG NGGNAAACAC GTGTTGTNTA 180
AGCCTTGNTG GNCTCGNAAG NGCCGTNGAC GCCTGTGTCG CCGAAGATAA TGAGCACCTG 240
ACGGTTGGCG CGATCGCCGT TATCCCAAGG AATTCCGAGG TCGGTCCCGG AGATGCCGAA 300
GCGTTCCAGG GTCTTGTTGG GGCTGTCCGG TCCGGTCACC CACTCGGCGA GGGATGTGGN 360
AGCCCCGGCG AGCGTGGCAC CAGGATCCGG CGCCGCCGCC GGAGCAGGGT CGGNNGCTGN 420
NCTGNNTTCC TNNNGCCNAA TTNNACTCCN NCNACAANCT TGNNNCCGAC TCNNACCCGN 480

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 597 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GCACGAGGCT ACCGGCGCGT CGCCCGCCAT GCCCTGGATG CACGCGTAGC CACCCGTNCA 60
TNCAGCGGGT CAGCCGCCGC GTCCGGGCTT AACGCTATAG CAGCTGCAAA CAACCCAGCG 120
CCGGCAATTA CTTTGATGTT GAACCGATGA CCATNGCCTN CGNGTNCAAT CTCNTCTCTT 180
NGCGCGCCNC TATTTNNGCC ATANATTTGG TTNNANNCGN AACGCTAGAC GTATCGAGTT 240

```
CCTTTTCGAC CACCGGCTCA ATTGTCAGCA TCCTATGGGG AACATGAGCC CCGCCGCACC    300
GGGCCGTTTC CAAATGGTGA CGTCACAACG GTGTCACAAG CCAGCGCAAT GTCCGCGGTA    360
GGGACGCGGC GGCTGGGATC GGTGGGGTGA GCGCCCGGCT TCTCAAAGCG AGGGGAGCCC    420
CGGGACTCTT ACCGGGCCGAA GGCGGCGGGT GTCACTGATC TAGGCTGACG GCCAGTGGTT    480
GNTNAGCCAA CAACGATGAC NACAAATAAN CCGAGGANAG ACANGNGACG GNCCGANANG    540
CTNANCCGGN NTTGNNCNAA NNNNACNCAC TTNTACCGNN CTTATGN                  587
```

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

```
CAGGCATGAG CAGAGCGTTC ATCATCGATC CAACGATCAG TGCCATTGAC GGCTTGTACG     60
ACCTTCTGGG GATTGGAATA CCCAACCAAG GGGGTATCCT TTACTCCTCA CTAGAGTACT    120
TCGAAAAAGC CCTGGAGGAG CTGGCAGCAG CGTTTCCGGG TGATGGCTGG TTAGGTTCGG    180
CCGCGGACAA ATACGCCGGC AAAAACCGCA ACCACGTGAA TTTTTTCCAG GAACTGGCAG    240
ACCTCGATCG TCAGCTCATC AGCCTGATCC ACGACCAGGC CAACCGCGTC CAGACGACCC    300
GCGACATCCT GGAGGGCGCC AAGAAAGGTC TCGAGTTCGT GCGCCCGGTG GCTGTGGACC    360
TGACCTACAT CCCGGTCGTC GGCCACGCCC TATCGGCCGC CTTCCAGGCG CCGTTTTGCG    420
CGGGCGCGAT GGCCGTAGTG GGCGGCGCGC TTGCCTACTT GGTCGTGAAA ACGCTGATCA    480
ACGCGACTCA ACTCCTCAAA TTGCTTGCCA AATTGGCGGA GTTGGTCGCG GCCGCCATTG    540
CGGACATCAT TTCGGATGTG GCGGACATCA TCAAGGCGAC CCTCGGACGA GTGTGGGAGT    600
TCATCACAAA CGCGCTCAAC GGCCTGAAAG AGCTTTGGGA CAAGCTCACG GGGTGGGTGA    660
CCGGACTGTT CTCTCGAGGG TGGTCGAACC TGGAGTCCTT CTTTGCGGGC GTCCCCGGCT    720
TGACCGGCGC GACCAGCGGC TTGTCGCAAG TGACTGGCTT GTTCGGTGCG GCCGGTCTGT    780
CCGCATCGTC GGGCTTGGCT CACGCGGATA GCCTGGCGAG CTCAGCCAGC TTGCCCGCCC    840
TGGCCGGCAT TGGGGGCGGG TCCGGTTTTG GGGGCTTGCC GAGCCTGGCT CAGGTCCATG    900
CCGCCTCAAC TCGGCAGGCG CTACGGCCCC GAGCTGATGG CCCGGTCGGC GCCGCTGCCG    960
AGCAGGTCGG CGGGCAGTCG CAGCTGGTCT CCGCGCAGGG TTCCCAAGGT ATGGGCGGAC   1020
CCGTAGGCAT GGGCGGCATG CACCCCTCTT CGGGGGCGTC GAAAGGGACG ACGACGAAGA   1080
AGTACTCGGA AGGCGCGGCG GCGGGCACTG AAGACGCCGA GCGCGCGCCA GTCGAAGCTG   1140
ACGCGGGCGG TGGGCAAAAG GTGCTGGTAC GAAACGTCGT CTAACGGCAT GGCGAGCCAA   1200
```

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 392 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```
Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
 1               5                  10                  15
Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
            20                  25                  30
Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
        35                  40                  45
```

```
Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
    50                  55                  60
Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
65                  70                  75                  80
Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
                85                  90                  95
Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
            100                 105                 110
Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
        115                 120                 125
Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
    130                 135                 140
Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
145                 150                 155                 160
Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
                165                 170                 175
Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
            180                 185                 190
Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
        195                 200                 205
Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
    210                 215                 220
Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
225                 230                 235                 240
Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
                245                 250                 255
Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
            260                 265                 270
Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
        275                 280                 285
Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
    290                 295                 300
Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
305                 310                 315                 320
Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
                325                 330                 335
Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
            340                 345                 350
Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
        355                 360                 365
Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
    370                 375                 380
Lys Val Leu Val Arg Asn Val Val
385                 390
```

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 439 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```
ACGTTTACCC ATGCCGTCGG TGCAGAGCAA CGCCAGACAA CACAAACTAG TCTAATTCCG      60
```

```
TTATAAAGCA GACATTTCCG TGGTTATGTA GAAGATGTCG ACCGATCAGA TGAAGCGATC    120
CGCGTCAGGT GGTATCCGAT GTCTTTTGTG ACCATCCAGC CGGTGGTCTT GGCAGCCGCG    180
ACGGGGGACT TGCCGACGAT CGGTACCGCC GTGAGTGCTC GGAACACAGC CGTCTGTGCC    240
CCGACGACGG GGGTGTTACC CCCTGCTGCC AATGACGTGT CGGTCCTGAC GGCGGCCCGG    300
TTCACCGCGC ACACCAAGCA CTACCGAGTG GTGAGTAAGC CGGCCGCGCT GGTCCATGGC    360
ATGTTCGTGG CCCTCCCGGC GGCCACCGCC GATGCGTATG CGACCACCGA GGCCGTCAAT    420
GTGGTCGCGA CCGGTTAAG                                                 439

(2) INFORMATION FOR SEQ ID NO:140:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1441 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: cDNA

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GAGGTTGCTG GCAATGGATT TCGGGCTTTT ACCTCCGGAA GTGAATTCAA GCCGAATGTA     60
TTCCGGTCCG GGGCCGGAGT CGATGCTAGC CGCCGCGGCC GCCTGGGACG GTGTGGCCGC    120
GGAGTTGACT TCCGCCGCGG TCTCGTATGG ATCGGTGGTG TCGACGCTGA TCGTTGAGCC    180
GTGGATGGGG CCGGCGGCGG CCGCGATGGC GGCCGCGGCA ACGCCGTATG TGGGGTGGCT    240
GGCCGCCACG GCGGCGCTGG CGAAGGAGAC GGCCACACAG GCGAGGGCAG CGGCGGAAGC    300
GTTTGGGACG GCGTTCGCGA TGACGGTGCC ACCATCCTC GTCGCGGCCA ACCGCAGCCG    360
GTTGATGTCG CTGGTCGCGG CGAACATTCT GGGGCAAAAC AGTGCGGCGA TCGCGGCTAC    420
CCAGGCCGAG TATGCCGAAA TGTGGGCCCA AGACGCTGCC GTGATGTACA GCTATGAGGG    480
GGCATCTGCG GCCGCGTCGG CGTTGCCGCC GTTCACTCCA CCCGTGCAAG GCACCGGCCC    540
GGCCGGGCCC GCGGCCGCAG CCGCGGCGAC CCAAGCCGCC GGTGCGGGCG CCGTTGCGGA    600
TGCACAGGCG ACACTGGCCC AGCTGCCCCC GGGGATCCTG AGCGACATTC TGTCCGCATT    660
GGCCGCCAAC GCTGATCCGC TGACATCGGG ACTGTTGGGG ATCGCGTCGA CCCTCAACCC    720
GCAAGTCGGA TCCGCTCAGC CGATAGTGAT CCCCACCCCG ATAGGGCAAT TGGACGTGAT    780
CGCGCTCTAC ATTGCATCCA TCGCGACCGC CAGCATTGCG CTCGCGATCA CGAACACGGC    840
CAGACCCTGG CACATCGGCC TATACGGGAA CGCCGGCGGC CTGGGACCGA CGCAGGGCCA    900
TCCACTGAGT TCGGCGACCG ACGAGCCGGA GCCGCACTGG GGCCCCTTCG GGGGCGCGGC    960
GCCGGTGTCC GCGGGCGTCG GCCACGCAGC ATTAGTCGGA GCGTTGTCGG TGCCGCACAG   1020
CTGGACCACG GCCGCCCCGG AGATCCAGCT CGCCGTTCAG GCAACACCCA CCTTCAGCTC   1080
CAGCGCCGGC GCCGACCCGA CGGCCCTAAA CGGGATGCCG GCAGGCCTGC TCAGCGGGAT   1140
GGCTTTGGCG AGCCTGGCCG CACGCGGCAC GACGGCGGT GGCGGCACCC GTAGCGGCAC   1200
CAGCACTGAC GGCCAAGAGG ACGGCGGCAA ACCCCCGGTA GTTGTGATTA GAGAGCAGCC   1260
GCCGCCCGGA AACCCCCCGC GGTAAAAGTC CGGCAACCGT TCGTCGCCGC GCGGAAAATG   1320
CCTGGTGAGC GTGGCTATCC GACGGGCGGT TCACACCGCT TGTAGTAGCG TACGGCTATG   1380
GACGACGGTG TCTGGATTCT CGGCGGCTAT CAGAGCGATT TTGCTCGCAA CCTCAGCAAA   1440
G                                                                   1441

(2) INFORMATION FOR SEQ ID NO:141:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 99 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:
```

```
Met Ser Phe Val Thr Ile Gln Pro Val Val Leu Ala Ala Ala Thr Gly
 1               5                  10                  15
Asp Leu Pro Thr Ile Gly Thr Ala Val Ser Ala Arg Asn Thr Ala Val
            20                  25                  30
Cys Ala Pro Thr Thr Gly Val Leu Pro Pro Ala Ala Asn Asp Val Ser
        35                  40                  45
Val Leu Thr Ala Ala Arg Phe Thr Ala His Thr Lys His Tyr Arg Val
    50                  55                  60
Val Ser Lys Pro Ala Ala Leu Val His Gly Met Phe Val Ala Leu Pro
65                  70                  75                  80
Ala Ala Thr Ala Asp Ala Tyr Ala Thr Thr Glu Ala Val Asn Val Val
                85                  90                  95
Ala Thr Gly
```

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 423 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```
Met Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr
 1               5                  10                  15
Ser Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Ala Trp Asp
            20                  25                  30
Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val
        35                  40                  45
Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala
    50                  55                  60
Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala
65                  70                  75                  80
Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala
                85                  90                  95
Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala
            100                 105                 110
Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln
        115                 120                 125
Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp
    130                 135                 140
Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala
145                 150                 155                 160
Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro
                165                 170                 175
Ala Gly Pro Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly
            180                 185                 190
Ala Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile
        195                 200                 205
Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr
    210                 215                 220
Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser
225                 230                 235                 240
Ala Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile
```

```
                    245                 250                 255
Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile
                260                 265                 270
Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly
            275                 280                 285
Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu
        290                 295                 300
Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala
305                 310                 315                 320
Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser
                325                 330                 335
Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro
            340                 345                 350
Thr Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met
        355                 360                 365
Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg
    370                 375                 380
Gly Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly
385                 390                 395                 400
Gln Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro
                405                 410                 415
Pro Pro Gly Asn Pro Pro Arg
            420
```

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```
Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
 1               5                  10                  15
Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
            20                  25                  30
Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
        35                  40                  45
Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys
    50                  55                  60
Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
65                  70                  75                  80
Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly
                85                  90                  95
Phe
```

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

```
Cys Arg Leu Cys Leu Asp Ser His Leu Arg Val Val Ala Leu Pro Ala
 1               5                  10                  15
Gly Gln Pro Gly Arg Leu Val Gln Ala Ile Gly Pro Ala Gln Glu Arg
            20                  25                  30
Asp Val Gly Gln Thr Arg Cys Thr Arg Thr Gly Leu Asp Xaa Val Ser
        35                  40                  45
Ala Leu Thr Ala Ala Gln Phe Ala Ala His Ala Gln Ile Tyr Gln Ala
    50                  55                  60
Val Ser Ala Gln Ala Ala Ala Ile His Glu Met Phe Val Asn Thr Leu
65                  70                  75                  80
Gln Xaa Xaa Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala Ala
                85                  90                  95
Ala Ala Gly
```

SF 1214848 v1